



#4

## SEQUENCE LISTING

&lt;110&gt; Cyclacel

&lt;120&gt; Compositions and Methods for Monitoring the Modification of Modification Dependent Binding Partner Polypeptides

&lt;130&gt; 10069/1062

&lt;140&gt; 09/770102

&lt;141&gt; 2001-01-25

&lt;150&gt; US 60/179283

&lt;151&gt; 2000-01-31

&lt;160&gt; 57

&lt;170&gt; PatentIn version 3.0

&lt;210&gt; 1

&lt;211&gt; 17

&lt;212&gt; PRT

&lt;213&gt; Unknown

&lt;220&gt;

&lt;223&gt; ADP-ribosylation domain

&lt;220&gt;

&lt;221&gt; DOMAIN

&lt;222&gt; (1)..(17)

&lt;223&gt; ADT-ribosylation site

&lt;400&gt; 1

Met	Leu	Cys	Cys	Met	Arg	Arg	Thr	Lys	Gln	Val	Glu	Lys	Asn	Asp	Asp
1				5				10				15			

Asp

&lt;210&gt; 2

&lt;211&gt; 10

&lt;212&gt; PRT

&lt;213&gt; Unknown

&lt;220&gt;

&lt;223&gt; ADP-ribosylation site

&lt;220&gt;

&lt;221&gt; DOMAIN

&lt;222&gt; (1)..(10)

&lt;223&gt; ADP-ribosylation site

&lt;400&gt; 2

Phe Lys Gln Arg Gln Thr Arg Gln Phe Lys  
1 5 10

<210> 3  
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<212> PRT  
<213> Unknown

<220>  
<223> ubiquitination site

<220>  
<221> DOMAIN  
<222> (1)..(30)  
<223> ubiquitination site

<400> 3

Met Phe Gln Ala Ala Glu Arg Pro Gln Glu Trp Ala Met Glu Gly Pro  
1 5 10 15

Arg Asp Gly Leu Lys Lys Glu Arg Leu Leu Asp Asp Arg His  
20 25 30

<210> 4  
<211> 21  
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<220>  
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<220>  
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<222> (1)..(21)  
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<400> 4

His Gly Ser Gly Ala Trp Leu Leu Pro Val Ser Leu Val Lys Arg Lys  
1 5 10 15

Thr Thr Leu Ala Pro  
20

<210> 5  
<211> 10  
<212> PRT  
<213> Unknown

<220>  
<223> O-GlcNAc site

<220>  
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<222> (1)..(10)  
<223> O-GlcNAc site

<400> 5

Gly Thr Thr Ser Thr Ile Gln Thr Ala Pro  
1 5 10

<210> 6  
<211> 12  
<212> PRT  
<213> Unknown

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<223> O-GlcNAc site

<220>  
<221> DOMAIN  
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<223> O-GlcNAc site

<400> 6

Ser Ala Val Ser Ser Ala Asp Gly Thr Val Leu Lys  
1 5 10

<210> 7  
<211> 18  
<212> PRT  
<213> Unknown

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<400> 7

Asp Ser Ser Thr Asp Leu Thr Gln Thr Ser Ser Ser Gly Thr Val Thr  
1 5 10 15

Leu Pro

<210> 8  
<211> 12  
<212> PRT  
<213> Unknown

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<400> 8

Met Ala Gly Gly Pro Ala Asp Thr Ser Asp Pro Leu  
1 5 10

<210> 9  
<211> 13  
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<213> Unknown

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<220>  
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<400> 9

Ala Gln Thr Ile Thr Ser Glu Thr Pro Ser Ser Thr Thr  
1 5 10

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<211> 8  
<212> PRT  
<213> Unknown

<220>  
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<222> (1)..(8)  
<223> X at position 3 may be any amino acid

<400> 10

Arg Arg Xaa Arg Arg Xaa Ser Thr  
1 5

<210> 11  
<211> 5  
<212> PRT  
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<223> Consensus sequence, each Xaa is any amino acid

<400> 11

Lys Xaa Xaa Ser Xaa  
1 5

<210> 12  
<211> 3  
<212> PRT  
<213> Unknown

<220>  
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<220>  
<221> DOMAIN  
<222> (1)..(3)  
<223> Consensus sequence, Xaa is any amino acid

<400> 12

Arg Xaa Thr  
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<210> 13  
<211> 5  
<212> PRT  
<213> Unknown

<220>  
<223> Consensus sequence

<220>  
<221> DOMAIN  
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<223> Consensus sequence, each Xaa is any amino acid

<400> 13

Arg Xaa Xaa Ser Xaa  
1 5

<210> 14  
<211> 4  
<212> PRT  
<213> Unknown

<220>  
<223> Consensus sequence

<220>  
<221> DOMAIN  
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<223> Consensus sequence, each Xaa is any amino acid

<400> 14

Xaa Ser Arg Xaa  
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<211> 8  
<212> PRT  
<213> Unknown

<220>  
<223> Consensus sequence

<220>  
<221> DOMAIN  
<222> (1)..(8)  
<223> Consensus sequence, each Xaa is any amino acid

<400> 15

Xaa Arg Xaa Xaa Ser Xaa Arg Xaa  
1 5

<210> 16  
<211> 6  
<212> PRT  
<213> Unknown

<220>  
<223> Consensus sequence

<220>  
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<223> Consensus sequence, each Xaa is any amino acid

<400> 16

Xaa Arg Xaa Xaa Ser Xaa  
1 5

<210> 17  
<211> 6  
<212> PRT  
<213> Unknown

<220>  
<223> Consensus sequence

<220>  
<221> DOMAIN  
<222> (1)..(6)  
<223> Consensus sequence

<400> 17

Ser Glu Leu Ser Arg Arg  
1 5

<210> 18  
<211> 6  
<212> PRT  
<213> Unknown

<220>  
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<220>  
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<223> Consensus sequence, each Xaa is any amino acid

<400> 18

Xaa Ser Xaa Xaa Ser Xaa  
1 5

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<213> Unknown

<220>  
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<220>  
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<223> Consensus sequence, each Xaa is any amino acid

<400> 19

Xaa Ser Xaa Glu Xaa  
1 5

<210> 20  
<211> 7  
<212> PRT  
<213> Unknown

<220>  
<223> Consensus sequence

<220>  
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<222> (1)..(7)  
<223> Consensus sequence, each Xaa is any amino acid

<400> 20

Xaa Ser Xaa Xaa Xaa Ser Xaa  
1 5

<210> 21  
<211> 9  
<212> PRT  
<213> Unknown

<220>  
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<220>  
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<222> (1)..(9)  
<223> Consensus sequence

<400> 21

Gly Ser Ser Lys Ser Lys Pro Lys Asp  
1 5

<210> 22  
<211> 9  
<212> PRT  
<213> Unknown

<220>  
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<221> DOMAIN  
<222> (1)..(9)  
<223> Consensus sequence

<400> 22

Gly Cys Ile Lys Ser Lys Arg Lys Asp  
1 5

<210> 23  
<211> 9  
<212> PRT  
<213> Unknown

<220>  
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<220>  
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<400> 23

Gly Cys Ile Lys Ser Lys Glu Asp Lys  
1 5

<210> 24  
<211> 9  
<212> PRT  
<213> Unknown

<220>  
<223> Consensus sequence

<220>  
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<222> (1)..(9)  
<223> Consensus sequence

<400> 24

Gly Cys Val Gln Cys Lys Asp Lys Glu  
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<210> 25  
<211> 9  
<212> PRT  
<213> Unknown

<220>  
<223> Consensus sequence

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<400> 25

Gly Cys Thr Leu Ser Ala Glu Asp Lys  
1 5

<210> 26  
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<212> PRT  
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<220>  
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<220>  
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<222> (1)..(9)  
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<400> 26

Gly Cys Ile Lys Ser Lys Arg Lys Asp  
1 5

<210> 27  
<211> 9  
<212> PRT  
<213> Unknown

<220>  
<223> Consensus sequence

<220>  
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<222> (1)..(9)  
<223> Consensus sequence

<400> 27

Gly Cys Val Gln Cys Lys Asp Lys Glu  
1 5

<210> 28  
<211> 9  
<212> PRT  
<213> Unknown

<220>  
<223> Consensus sequence

<220>  
<221> DOMAIN  
<222> (1)..(9)  
<223> Consensus sequence

<400> 28

Gly Cys Thr Leu Ser Ala Glu Asp Lys  
1 5

<210> 29  
<211> 4  
<212> PRT  
<213> Unknown

<220>  
<223> Consensus sequence

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<220>
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<222> (1)..(4)
<223> Consensus sequence, Xaa is any amino acid

<400> 29

Asn Xaa Ser Thr
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<210> 30
<211> 4
<212> PRT
<213> Unknown

<220>
<223> C-terminal sequence

<220>
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<222> (1)..(4)
<223> C-terminal sequence

<400> 30

His Ser Thr Val
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<210> 31
<211> 92
<212> DNA
<213> Artificial

<220>
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<220>
<221> misc_feature
<222> (1)..(92)
<223> Synthetic primer

<400> 31
ggggggagct ctgggaggcg gaggtggagg gctgatgcgc cagctgcagg atgaagttga      60
agaactggaa cagaaaaact ggcatctgca ga                                92

<210> 32
<211> 96
<212> DNA
<213> Artificial

<220>

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<223> Synthetic primer .

<220>  
<221> misc\_feature  
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<223> Synthetic primer

<400> 32  
ccccccctcga gttattaaac ttccggcttcc aggcaactgaa cttcacgcag cagacgggca 60  
acttcgttct gcagatgcca gttttcctgt tccagt 96

<210> 33  
<211> 37  
<212> PRT  
<213> Unknown

<220>  
<223> Coiled-coil sequence

<220>  
<221> DOMAIN  
<222> (1)..(37)  
<223> Coiled coil sequence

<400> 33

Leu Met Arg Gln Leu Gln Asp Glu Val Glu Glu Leu Glu Gln Glu Asn  
1 5 10 15

Trp His Leu Gln Asn Glu Val Ala Arg Leu Leu Arg Glu Val Gln Cys  
20 25 30

Leu Glu Ala Glu Val  
35

<210> 34  
<211> 37  
<212> PRT  
<213> Unknown

<220>  
<223> Coiled coil sequence

<220>  
<221> DOMAIN  
<222> (1)..(37)  
<223> Coiled coil sequence

<400> 34

Arg Met Arg Gln Leu Glu Asp Arg Val Glu Glu Leu Arg Glu Gln Asn  
1 5 10 15

Trp His Leu Ala Asn Gln Val Ala Arg Leu Arg Gln Arg Val Cys Glu  
 20 25 30

Leu Lys Ala Arg Val  
 35

<210> 35  
 <211> 80  
 <212> DNA  
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<220>  
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<220>  
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 <222> (1)..(80)  
 <223> Synthetic primer

<400> 35  
 gtaccgctag ctcttacaag ggtattgctc agttggagca ggaaatcgcc caattagaac 60  
 aagaaaaatgc acaacttgaa 80

<210> 36  
 <211> 73  
 <212> DNA  
 <213> Artificial

<220>  
 <223> Synthetic primer

<220>  
 <221> misc\_feature  
 <222> (1)..(61)  
 <223> Synthetic primer

<400> 36  
 gggcatcgat ttcctgctca agctgagcga tctcttgttc aagttgtgca ttttcttgtt 60  
 ctaattgggc gat 73

<210> 37  
 <211> 31  
 <212> PRT  
 <213> Unknown

<220>  
 <223> Sequence for cloning

<220>  
 <221> DOMAIN

<222> (1)..(31)  
<223> Sequence for cloning

<400> 37

Tyr Lys Gly Ile Ala Gln Leu Glu Gln Glu Ile Ala Gln Leu Glu Gln  
1 5 10 15

Glu Asn Ala Gln Leu Glu Gln Glu Ile Ala Gln Leu Glu Gln Glu  
20 25 30

<210> 38

<211> 38

<212> PRT

<213> Unknown

<220>

<223> Coiled coil sequence

<220>

<221> DOMAIN

<222> (1)..(38)

<223> Coiled coil sequence

<400> 38

Tyr Lys Gly Ile Cys Gln Leu Arg Gln Arg Ile Ala Gln Leu Arg Gln  
1 5 10 15

Arg Asn Ala Gln Leu Arg Gln Arg Ile Ala Gln Leu Arg Gln Arg Ile  
20 25 30

Ala Gln Leu Arg Gln Arg  
35

<210> 39

<211> 36

<212> PRT

<213> Artificial

<220>

<223> Synthetic peptide

<220>

<221> PEPTIDE

<222> (1)..(36)

<223> Synthetic peptide

<400> 39

Arg Cys Lys Phe Ser Arg Ser Ala Glu Pro Pro Ala Tyr Gln Gln Gly  
1 5 10 15

Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr

20

25

30

Asp Val Leu Asp  
35

<210> 40  
<211> 36  
<212> PRT  
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<220>  
<223> Synthetic peptide

<220>  
<221> PEPTIDE  
<222> (1)..(36)  
<223> Synthetic peptide

<400> 40

Arg Cys Lys Phe Ser Arg Ser Ala Glu Pro Pro Ala Tyr Gln Gln Gly  
1 5 10 15

Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr  
20 25 30

Asp Val Leu Asp  
35

<210> 41  
<211> 33  
<212> DNA  
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<220>  
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<222> (1)..(33)  
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<400> 41  
gggatccata tgccagaccc cgccggcgac ctg

33

<210> 42  
<211> 33  
<212> DNA  
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<220>  
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<220>

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<222> (1)..(33)  
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<400> 42  
ggaattcggg cactgctgtt gggcaggcc tcc

33

<210> 43  
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<400> 43  
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23

<210> 44  
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<220>  
<223> Synthetic primer

<220>  
<221> misc\_feature  
<222> (1)..(23)  
<223> Synthetic primer

<400> 44  
ggggcccgag gcccccccgac tac

23

<210> 45  
<211> 23  
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<220>  
<223> Synthetic primer

<220>  
<221> misc\_feature  
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<223> Synthetic primer

<400> 45  
gggggccccaa ccagctctat aac

23

<210> 46  
<211> 23  
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<400> 46  
ggggatccgc gagggggcag ggc

23

<210> 47  
<211> 36  
<212> PRT  
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<220>  
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<222> (1)..(36)  
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<400> 47

Arg Cys Lys Phe Ser Arg Ser Ala Glu Pro Pro Ala Tyr Gln Gln Gly  
1 5 10 15

Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr  
20 25 30

Asp Val Leu Asp  
35

<210> 48  
<211> 6  
<212> PRT  
<213> Unknown  
  
<220>  
<223> Cleavage site

<220>  
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<222> (1)..(6)  
<223> Xaa is any amino acid

<400> 48

Trp Leu Glu His Asp Xaa  
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<210> 49  
<211> 5  
<212> PRT  
<213> Unknown

<220>  
<223> Cleavage site

<220>  
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<222> (1)..(5)  
<223> Cleavage site, each Xaa is any amino acid

<400> 49

Asp Glu Xaa Asp Xaa  
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<210> 50  
<211> 6  
<212> PRT  
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<220>  
<223> Cleavage site

<220>  
<221> SITE  
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<223> Cleavage site, Xaa is any amino acid

<400> 50

Leu Val Glu Xaa Asp Xaa  
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<210> 51  
<211> 5  
<212> PRT  
<213> Unknown

<220>  
<223> Cleavage site

<220>  
<221> SITE  
<222> (1)..(5)  
<223> Cleavage site, Xaa is any amino acid

<400> 51

Ile Glu Gly Arg Xaa  
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<210> 52  
<211> 8  
<212> PRT  
<213> Unknown

<220>  
<223> Cleavage site

<220>  
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<223> Cleavage site, each Xaa is any amino acid

<400> 52

Glu Asn Xaa Tyr Xaa Gln Ser Gly  
1 5

<210> 53  
<211> 5  
<212> PRT  
<213> Artificial

<220>  
<223> Tag peptide

<220>  
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<400> 53

Arg Tyr Ile Arg Ser  
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<210> 54  
<211> 6  
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<400> 54

Asp Thr Tyr Arg Tyr Ile  
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<210> 55  
<211> 6  
<212> PRT  
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<220>  
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<220>  
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<400> 55

Thr Asp Phe Leu Tyr Lys  
1 5

<210> 56  
<211> 9  
<212> PRT  
<213> Artificial

<220>  
<223> Tag peptide

<220>  
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<222> (1)..(9)  
<223> Tag sequence

<400> 56

Glu Glu Glu Glu Tyr Met Pro Met Glu  
1 5

<210> 57  
<211> 11  
<212> PRT  
<213> Artificial

<220>  
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<220>  
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<222> (1)..(11)  
<223> Tag sequence

<400> 57

Lys Pro Pro Thr Pro Pro Pro Glu Pro Glu Thr  
1 5 10